

## RAW SEQUENCE LISTING

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Application Serial Number: 10/529,381

Source: PCT

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# ENTERED

ATTN: KAREN



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/529,381

DATE: 09/21/2005  
TIME: 14:25:34

Input Set : N:\CrF4\Refhold\10\_folder\J529381.raw  
Output Set: N:\CRF4\09212005\J529381.raw

1 <110> APPLICANT: Nakamura, Yusuke  
2 Katagiri, Toyomasa  
3 Nakagawa, Hidewaki  
4 Nakatsuru, Shuichi  
5 Oncotherapy Science, Inc.  
6 The University of Tokyo  
7 <120> TITLE OF INVENTION: GENES AND POLYPEPTIDES RELATING TO  
8 PROSTATE CANCERS  
9 <130> FILE REFERENCE: 082368-002810US  
10 <140> CURRENT APPLICATION NUMBER: US/10/529,381  
11 <141> CURRENT FILING DATE: 2005-03-28  
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/12074  
13 <151> PRIOR FILING DATE: 2003-09-22  
14 <150> PRIOR APPLICATION NUMBER: US 60/414,873  
15 <151> PRIOR FILING DATE: 2002-09-30  
16 <160> NUMBER OF SEQ ID NOS: 28  
17 <170> SOFTWARE: PatentIn version 3.1  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 826  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (332)..(634)  
25 <223> OTHER INFORMATION:  
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30 aaaaggatca cagatggaga gacatggc cacacgatga atcacacaccc acatctcatc 180  
31 cccgagcttc agctgcagga caatgctgcc agaggcctgg tcctcagagc tcacgtaagc 240  
32 atctctggtg tgcagtatcc ttactccgtt tttgaccaaa gacacctgaa cattcctgga 300  
33 gaaaacagtgc atgtggatct tatcaaattt a atg ggc aca tct gaa gaa gga 352  
34 Met Gly Thr Ser Glu Glu Gly  
35 1 5  
36 aac ttg ctc agc acc gtg agc ccc aca gtg aaa gca ctt ttt ggc aag 400  
37 Asn Leu Leu Ser Thr Val Ser Pro Thr Val Lys Ala Leu Phe Gly Lys  
38 10 15 20  
39 act aga gtc tca ccg att ttc cct tct cct cga tot cct ttc cag 448  
40 Thr Arg Val Ser Pro Ile Phe Pro Phe Ser Pro Arg Ser Pro Phe Gln  
41 25 30 35  
42 cct ctt att ccc cgg act cct ggc tca ccc tgg ggc ccc gtg ggt cca 496  
43 Pro Leu Ile Pro Arg Thr Pro Gly Ser Pro Trp Gly Pro Val Gly Pro  
44 40 45 50 55

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45	gct tct ccc ttg gga cca ggc ttt cca ata ggg ccc atg ggg ccc ggt	544
46	Ala Ser Pro Leu Gly Pro Gly Phe Pro Ile Gly Pro Met Gly Pro Gly	
47	60 65 70	
48	aaa cca gtt ggg ccc aaa ggc cca atg ttg ccc ctt ggc ccc tca gga	592
49	Lys Pro Val Gly Pro Lys Gly Pro Met Leu Pro Leu Gly Pro Ser Gly	
50	75 80 85	
51	cca gtg gga ccc acg tca ccc tta ttc ccc ttc tgc ccc tga	634
52	Pro Val Gly Pro Thr Ser Pro Leu Phe Pro Phe Cys Pro	
53	90 95 100	
54	ggcccaagtct ctcctcgag gcatttatct cccatggggcc ctgcaagccctt cttggggccca	694
55	tgttttcctg gggatccctct tgagccttga tcacctttga tgccctttgc ttcaactttt	754
56	ccatctgtct ctaaatagag aaagagccaa taaagagata gtttgtaaaaa gataaaaaaaa	814
57	aaaaaaaaaa aa	826
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60 <211>	LENGTH: 100	
61 <212>	TYPE: PRT	
62 <213>	ORGANISM: Homo sapiens	
63 <400>	SEQUENCE: 2	
64	Met Gly Thr Ser Glu Glu Gly Asn Leu Leu Ser Thr Val Ser Pro Thr	
65	1 5 10 15	
66	Val Lys Ala Leu Phe Gly Lys Thr Arg Val Ser Pro Ile Phe Pro Phe	
67	20 25 30	
68	Ser Pro Arg Ser Pro Phe Gln Pro Leu Ile Pro Arg Thr Pro Gly Ser	
69	35 40 45	
70	Pro Trp Gly Pro Val Gly Pro Ala Ser Pro Leu Gly Pro Gly Phe Pro	
71	50 55 60	
72	Ile Gly Pro Met Gly Pro Gly Lys Pro Val Gly Pro Lys Gly Pro Met	
73	65 70 75 80	
74	Leu Pro Leu Gly Pro Ser Gly Pro Val Gly Pro Thr Ser Pro Leu Phe	
75	85 90 95	
76	Pro Phe Cys Pro	
77	100	
79 <210>	SEQ ID NO: 3	
80 <211>	LENGTH: 6805	
81 <212>	TYPE: DNA	
82 <213>	ORGANISM: Homo sapiens	
83 <220>	FEATURE:	
84 <221>	NAME/KEY: CDS	
85 <222>	LOCATION: (265)..(3195)	
86 <223>	OTHER INFORMATION:	
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89	cgccggccagg gcccggccagg gcctgaccccg gggccggccaa gcccggccggaa ctttcggaaac	120
90	atggcaaccc gtgtgtgtct catcccagaa agagaagact ttaaccactg tgatgctga	180
91	gaatccagtg tgacgtttct ccagatactt catgtgttcc acctgtgtcc tcggccgacc	240
92	actgcccggaa acgactcctg aacc atg ggg gaa aac gag gat gag aag cag	291
93	Met Gly Glu Asn Glu Asp Glu Lys Gln	
94	1 5	
95	gcc cag gcg ggg cag gtt ttt gag aac ttc gtc cag gca tcc acg tgc	339

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96	Ala Gln Ala Gly Gln Val Phe Glu Asn Phe Val Gln Ala Ser Thr Cys	
97	15 20 25	
98	aaa ggt acc ctc cag gcc ttc aac att ctc aca cga cac ctg gac cta	387
99	Lys Gly Thr Leu Gln Ala Phe Asn Ile Leu Thr Arg His Leu Asp Leu	
100	30 35 40	
101	gac cct ctg gac cac aga aac aac ttt tat tcc aag ctc aag tcc aag gtg	435
102	Asp Pro Leu Asp His Arg Asn Phe Tyr Ser Lys Leu Lys Ser Lys Val	
103	45 50 55	
104	acc acc tgg aaa gcc aaa gcc ctg tgg tac aaa ttg gat aag cgt ggt	483
105	Thr Thr Trp Lys Ala Lys Ala Leu Trp Tyr Lys Leu Asp Lys Arg Gly	
106	60 65 70	
107	tcc cac aaa gag tat aag cga ggg aag tcg tgc acg aac acc aag tgt	531
108	Ser His Lys Glu Tyr Lys Arg Gly Lys Ser Cys Thr Asn Thr Lys Cys	
109	75 80 85	
110	ctc ata gtt ggg gga gga ccc tgt ggc ttg cgc act gcc att gaa ctt	579
111	Leu Ile Val Gly Gly Pro Cys Gly Leu Arg Thr Ala Ile Glu Leu	
112	90 95 100 105	
113	gcc tac ctg gga gcc aaa gtg gtc gtg gtg gag aag agg gac tcc ttc	627
114	Ala Tyr Leu Gly Ala Lys Val Val Val Val Glu Lys Arg Asp Ser Phe	
115	110 115 120	
116	tcc cgg aac aac gtg cta cac ctc tgg cct ttc acc atc cat gac ctt	675
117	Ser Arg Asn Asn Val Leu His Leu Trp Pro Phe Thr Ile His Asp Leu	
118	125 130 135	
119	cgg ggc ctg gga gcc aag aag ttc tat ggg aag ttc tgt gct ggc tcc	723
120	Arg Gly Leu Gly Ala Lys Lys Phe Tyr Gly Lys Phe Cys Ala Gly Ser	
121	140 145 150	
122	atc gac cat atc agt att cgc caa cta cag ctc atc cta ttc aag gtg	771
123	Ile Asp His Ile Ser Ile Arg Gln Leu Gln Leu Ile Leu Phe Lys Val	
124	155 160 165	
125	gcc ctg atg ctg gga gtt gaa atc cat gtg aat gtg gag ttc gtg aag	819
126	Ala Leu Met Leu Gly Val Glu Ile His Val Asn Val Glu Phe Val Lys	
127	170 175 180 185	
128	gtt cta gag cct cct gaa gat caa gaa aat caa aaa att ggc tgg cgg	867
129	Val Leu Glu Pro Pro Glu Asp Gln Glu Asn Gln Lys Ile Gly Trp Arg	
130	190 195 200	
131	gca gaa ttt ctc cct aca gac cat tct ctg tcg gag ttt gag ttt gac	915
132	Ala Glu Phe Leu Pro Thr Asp His Ser Leu Ser Glu Phe Glu Phe Asp	
133	205 210 215	
134	gtc atc att ggt gcc gat ggc cgc agg aac acc ctg gaa ggg ttc aga	963
135	Val Ile Ile Gly Ala Asp Gly Arg Arg Asn Thr Leu Glu Gly Phe Arg	
136	220 225 230	
137	aga aaa gaa ttc cgt ggg aag ctg gcg att gcc atc acc gcc aac ttc	1011
138	Arg Lys Glu Phe Arg Gly Lys Leu Ala Ile Ala Ile Thr Ala Asn Phe	
139	235 240 245	
140	ata aac aga aac agc aca gcg gaa aag gtg gaa gag att agt ggt	1059
141	Ile Asn Arg Asn Ser Thr Ala Glu Ala Lys Val Glu Glu Ile Ser Gly	
142	250 255 260 265	
143	gtg gct ttc atc ttc aat cag aaa ttt ttt cag gac ctt aaa gaa gaa	1107
144	Val Ala Phe Ile Phe Asn Gln Lys Phe Phe Gln Asp Leu Lys Glu Glu	

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145	270	275	280		
146	aca ggc ata gat ctt gag aac att gtt tac tac aag gac tgc acc cac			1155	
147	Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys Asp Cys Thr His				
148	285	290	295		
149	tat ttt gta atg aca gcc aag aag cag agc ctg ctc gac aaa ggt gtc			1203	
150	Tyr Phe Val Met Thr Ala Lys Lys Gln Ser Leu Leu Asp Lys Gly Val				
151	300	305	310		
152	atc att aac gac tac atc gac aca gag atg ctg ctg tgc gag aac			1251	
153	Ile Ile Asn Asp Tyr Ile Asp Thr Glu Met Leu Leu Cys Ala Glu Asn				
154	315	320	325		
155	gtg aac caa gac aac ctg cta tcc tat gcc cgg gaa gct gca gac ttt			1299	
156	Val Asn Gln Asp Asn Leu Leu Ser Tyr Ala Arg Glu Ala Ala Asp Phe				
157	330	335	340	345	
158	gcc acc aac tac cag ctg cca tcc tta gac ttt gcc atg aac cac tat			1347	
159	Ala Thr Asn Tyr Gln Leu Pro Ser Leu Asp Phe Ala Met Asn His Tyr				
160	350	355	360		
161	ggg cag cct gat gtg gcc atg ttt gac ttt acc tgc atg tat gcc tca			1395	
162	Gly Gln Pro Asp Val Ala Met Phe Asp Phe Thr Cys Met Tyr Ala Ser				
163	365	370	375		
164	gag aac gcg gcc ctg gtg cgg gag cgg cag gac ctg ctc gtg			1443	
165	Glu Asn Ala Ala Leu Val Arg Glu Arg Gln Ala His Gln Leu Leu Val				
166	380	385	390		
167	gcc ctt gtg ggt gac agc ttg ctt gag cca ttt tgg ccc atg ggt aca			1491	
168	Ala Leu Val Gly Asp Ser Leu Leu Glu Pro Phe Trp Pro Met Gly Thr				
169	395	400	405		
170	ggc tgt gcc cgt ggc ttc ctg gca gcc ttt gac acg gca tgg atg gtg			1539	
171	Gly Cys Ala Arg Gly Phe Leu Ala Ala Phe Asp Thr Ala Trp Met Val				
172	410	415	420	425	
173	aag agc tgg aac cag ggc acc cct ccc ctg gag ctg ctg gct gaa agg			1587	
174	Lys Ser Trp Asn Gln Gly Thr Pro Pro Leu Glu Leu Leu Ala Glu Arg				
175	430	435	440		
176	gaa agt ctc tac cgg ctg tta cct cag aca acc ccc gag aac atc aac			1635	
177	Glu Ser Leu Tyr Arg Leu Leu Pro Gln Thr Thr Pro Glu Asn Ile Asn				
178	445	450	455		
179	aag aac ttt gag cag tac acg ttg gac cca ggg aca cgg tac cca aac			1683	
180	Lys Asn Phe Glu Gln Tyr Thr Leu Asp Pro Gly Thr Arg Tyr Pro Asn				
181	460	465	470		
182	ctc aac tca cac tgt gtc agg ccc cat cag gtg aag cat ttg tat atc			1731	
183	Leu Asn Ser His Cys Val Arg Pro His Gln Val Lys His Leu Tyr Ile				
184	475	480	485		
185	act aag gag ctg gag cac tac ccc gag aga ctg ggc tgc gtg agg			1779	
186	Thr Lys Glu Leu Glu His Tyr Pro Leu Glu Arg Leu Gly Ser Val Arg				
187	490	495	500	505	
188	aga tct gtc aac ctc tcc agg aag gag tca gat atc cgg ccc agc aag			1827	
189	Arg Ser Val Asn Leu Ser Arg Lys Glu Ser Asp Ile Arg Pro Ser Lys				
190	510	515	520		
191	ctc ctg acc tgg tgc cag cag cag aca gag ggc tac cag cat gtc aac			1875	
192	Leu Leu Thr Trp Cys Gln Gln Thr Glu Gly Tyr Gln His Val Asn				
193	525	530	535		

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194	gtc acc gac ctg acc aca tcc tgg cgc agt ggg ttg gcc ctg tgt gcc	1923
195	Val Thr Asp Leu Thr Ser Trp Arg Ser Gly Leu Ala Leu Cys Ala	
196	540 545 550	
197	atc atc cac cgc ttc cgg cct gag ctc atc aac ttt gac tct ttg aat	1971
198	Ile Ile His Arg Phe Arg Pro Glu Leu Ile Asn Phe Asp Ser Leu Asn	
199	555 560 565	
200	gaa gat gat gct gtg gag aac aac cag ctc gca ttt gat gtg gcc gag	2019
201	Glu Asp Asp Ala Val Glu Asn Asn Gln Leu Ala Phe Asp Val Ala Glu	
202	570 575 580 585	
203	cga gag ttt ggg atc cct cca gtg acc acg ggc aaa gag atg gca tct	2067
204	Arg Glu Phe Gly Ile Pro Pro Val Thr Thr Gly Lys Glu Met Ala Ser	
205	590 595 600	
206	gcc cag gag cct gac aag ctc agc atg gtc atg tac ctc tcc aag ttc	2115
207	Ala Gln Glu Pro Asp Lys Leu Ser Met Val Met Tyr Leu Ser Lys Phe	
208	605 610 615	
209	tac gag ctc ttc cgg ggc acc cca ctg agg ccc gtg gat tct tgg cgc	2163
210	Tyr Glu Leu Phe Arg Gly Thr Pro Leu Arg Pro Val Asp Ser Trp Arg	
211	620 625 630	
212	aaa aac tat gga gaa aat gct gac ctc agc ttg gcc aaa tca tcc att	2211
213	Lys Asn Tyr Gly Glu Asn Ala Asp Leu Ser Leu Ala Lys Ser Ser Ile	
214	635 640 645	
215	tct aat aac tat ctc aac ctc aca ttt cca agg aag agg act cca cgg	2259
216	Ser Asn Asn Tyr Leu Asn Leu Thr Phe Pro Arg Lys Arg Thr Pro Arg	
217	650 655 660 665	
218	gtg gat ggt caa acc gga gag aat gac atg aac aaa cgg aga cgg aag	2307
219	Val Asp Gly Gln Thr Gly Glu Asn Asp Met Asn Lys Arg Arg Arg Lys	
220	670 675 680	
221	ggc ttc acc aac ctg gac gag cct tca aac ttt tcc agc cgt agc ttg	2355
222	Gly Phe Thr Asn Leu Asp Glu Pro Ser Asn Phe Ser Ser Arg Ser Leu	
223	685 690 695	
224	ggc tcc aat caa gag tgt ggg agc agt aag gaa ggt gga aat cag aac	2403
225	Gly Ser Asn Gln Glu Cys Gly Ser Ser Lys Glu Gly Asn Gln Asn	
226	700 705 710	
227	aaa gtc aag tcc atg gcg aat cag ctg ctg gcc aag ttt gag gag agc	2451
228	Lys Val Lys Ser Met Ala Asn Gln Leu Leu Ala Lys Phe Glu Glu Ser	
229	715 720 725	
230	act cgg aac ccc tca ctc atg aag cag gaa aag tca cct tca ggg	2499
231	Thr Arg Asn Pro Ser Leu Met Lys Gln Glu Lys Lys Ser Pro Ser Gly	
232	730 735 740 745	
233	ttc cat ttt cat ccc agc cat ttg aga aca gtg cat cct cag gaa tct	2547
234	Rhe His Phe His Pro Ser His Leu Arg Thr Val His Pro Gln Glu Ser	
235	750 755 760	
236	atg cga aag tca ttt ccc ctt aac ctg gga ggc agc gac acg tgt tac	2595
237	Met Arg Lys Ser Phe Pro Leu Asn Leu Gly Gly Ser Asp Thr Cys Tyr	
238	765 770 775	
239	ttc tgt aag aaa cgt gtg tac gtg atg gaa cgg ctg agc gac gcc gag ggc	2643
240	Phe Cys Lys Lys Arg Val Tyr Val Met Glu Arg Leu Ser Ala Glu Gly	
241	780 785 790	
242	cac ttc ttc cac cgg gag tgt ttc cgc tgc agc atc tgt gcc acc acc	2691

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/21/2005  
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Invalid <213> Response:  
Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28

## VERIFICATION SUMMARY

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Input Set : N:\Crf4\Refhold\10\_folder\J529381.raw  
Output Set: N:\CRF4\09212005\J529381.rawL:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0  
L:87 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0  
L:475 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0